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Abstract

Differences between porcine stress syndrome (PSS) normal (NN) and carrier (Nn) Landrace dams were determined for adjusted number of pigs born alive, adjusted number of pigs at 21 d, adjusted 21-d litter weight, proportion of pigs surviving to 21 d, and farrowing interval. Data were analyzed from a total of 841 females, 623 normal (NN) and 218 carriers (Nn) having 2,231 and 869 records, respectively. Three susceptible (nn) females from two herds were dropped from the analysis because of their small contribution to the total number of records. Frequency of the recessive PSS allele ranged from .07 to .28 in the nine herds involved in this study. Data were adjusted using Landrace breed-specific adjustments and analyzed with mixed-model derivative-free REML procedures fitting the dams' PSS genotype as a fixed effect in the model. Only females having two or more successive parities were used in the analysis of farrowing interval, resulting in a reduction of total records analyzed to 2,201 (1,564 NN and 637 Nn records) from 632 females (445 NN and 187 Nn females). No differences between NN and Nn dams were observed for adjusted number of pigs born alive, adjusted number of pigs at 21 d, adjusted 21-d litter weight, proportion of pigs surviving to 21 d, and farrowing interval. The results of this investigation indicate no significant maternal performance differences between PSS NN or Nn Landrace dams.

Keywords

Pigs, Stress, Reproductive Performance

Disciplines

Agriculture | Animal Sciences

Comments

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Maternal Performance Differences Between Porcine Stress Syndrome-Normal and -Carrier Landrace Females^{1,2}

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ABSTRACT: Differences between porcine stress syndrome (PSS) normal (NN) and carrier (Nn) Landrace dams were determined for adjusted number of pigs born alive, adjusted number of pigs at 21 d, adjusted 21-d litter weight, proportion of pigs surviving to 21 d, and farrowing interval. Data were analyzed from a total of 841 females, 623 normal (NN) and 218 carriers (Nn) having 2,231 and 869 records, respectively. Three susceptible (nn) females from two herds were dropped from the analysis because of their small contribution to the total number of records. Frequency of the recessive PSS allele ranged from .07 to .28 in the nine herds involved in this study. Data were adjusted using Landrace breed-

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Key Words: Pigs, Stress, Reproductive Performance

J. Anim. Sci. 1997. 75:3114-3118

Introduction

The profitability of commercial and seedstock swine operations is heavily influenced by the reproductive performance of breeding herd females (Mabry et al., 1990). Some commercial swine producers have used porcine stress syndrome (PSS) carrier (Nn) or positive (nn) sires to produce leaner market hogs. Many swine producers still raise their own replacement females. The potential exists for increasing the frequency of the PSS positive allele (n) in breeding herds if producers use Nn and nn terminal sires and raise their own replacement females.

Effects of PSS on maternal traits has largely been ignored since its discovery by Topel et al. (1968). Advances in molecular biology led to a molecular DNA test (Fujii et al., 1991) to determine the PSS genotype of individual pigs. This simple and cost-effective procedure allows swine producers to classify individual pigs into one of the three PSS genotypes with an accuracy approaching 100%. Swine producers should use all available information to make an informative decision concerning the proper use of the PSS gene in their breeding programs. The objective of this study was to determine maternal performance differences at birth and 21 d between PSS-NN and -Nn Landrace females.

Materials and Methods

Animals

Nine purebred Landrace herds from across the United States provided the registration number and PSS genotype of each female within their herd. These herds were selected because the PSS genotype of all current breeding females was known. Porcine stress syndrome genotypes were determined by commercial laboratories using the DNA molecular procedure

¹Journal paper no. J-17029 of the Iowa Agric. and Home Econ. Exp. Sta., Ames. Project no. 3043, and supported by Hatch Act and State of Iowa funds.

²The authors gratefully acknowledge the American Landrace Association, West Lafayette, IN and participating Landrace breeders for providing data used in this study.

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Received December 11, 1996.

Accepted July 13, 1997.

Table 1. Frequency of the porcine stress syndrome (PSS) gene (*n*), distribution of total sows and (records), and distribution of sows with two or more consecutive records by herd and porcine stress syndrome genotype

Herd	Frequency of the PSS <i>n</i> allele	Distribution of sows (records) by genotype ^a				Distribution of sows with two or more consecutive records ^b by genotype		
		NN	Nn	nn	Total	NN	Nn	Total
1	.11	28 (131)	8 (49)	0	36 (180)	24 (103)	8 (41)	32 (144)
2	.17	28 (157)	14 (90)	0	42 (247)	27 (128)	14 (76)	41 (204)
3	.15	135 (472)	57 (257)	1 (9)	193 (729)	85 (329)	53 (192)	138 (521)
4	.13	173 (848)	62 (277)	0	235 (1,125)	163 (656)	60 (210)	223 (866)
5	.08	60 (95)	12 (22)	0	72 (117)	27 (31)	8 (9)	35 (40)
6	.07	52 (172)	9 (29)	0	61 (201)	42 (116)	8 (19)	50 (135)
7	.13	28 (52)	10 (25)	0	38 (77)	15 (24)	7 (15)	22 (39)
8	.28	22 (74)	25 (70)	2 (4)	49 (144)	18 (49)	20 (47)	38 (96)
9	.09	97 (230)	21 (50)	0	118 (280)	44 (128)	9 (28)	53 (156)
Total	.13	623 (2,231)	218 (869)	3 (13)	844 (3,113)	445 (1,564)	187 (367)	632 (2,201)

^aRecessive (nn) sows and their records were dropped from analyses because of insufficient number of records to adequately evaluate sows possessing this PSS genotype.

^bNumber of sows and records involved in the analysis of farrowing interval.

described by Fujii et al. (1991). The procedure can detect the presence of the recessive allele responsible for a defect in the calcium-release channel resulting in improper regulation of calcium release from the sarcoplasmic reticulum and the PSS condition (Knudson et al., 1990).

Records from a total of 844 sows (623 NN, 218 Nn, and 3 nn females) with known PSS genotypes were provided by these nine herds. The smallest herd provided records for 36 sows, and the largest herd provided records for 235 sows. Frequency of the PSS positive allele was calculated for each herd and across all herds (Table 1). The distribution of females and corresponding number of records by herd and genotype are presented in Table 1.

Data Description

Sow productivity records and registration numbers were obtained from the American Landrace Association (ALA) and merged with the PSS genotypes provided by the various Landrace breeders. In total, 3,113 records (2,231 NN, 869 Nn, and 13 nn) were obtained (Table 1). The three nn dams and their records were dropped from the analysis because of an insufficient number of records to adequately evaluate dams possessing this PSS genotype. The maternal litter information provided by the ALA included number of pigs born alive (NBA), number of pigs nursing each female after cross-fostering had occurred 1 to 3 d after farrowing (NAT), number of pigs at 21 d (NO21), and litter weight taken at approximately 21 d (LWT21). The proportion of pigs surviving from transfer to 21 d (SURV21) was calculated from the data provided by the ALA. Additionally, farrowing interval between two consecutive parities was calculated. In all, 2,201 records from 632 sows (Table 1) were evaluated in the analysis of farrowing interval.

Statistical Analyses

Landrace breed-specific adjustments for parity, NAT, and age at weighing (Brubaker et al., 1994) were applied to NBA, NO21, and LWT21 before the analysis of these traits. All reproductive data were analyzed by using the full animal model described as follows:

$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}_1\mathbf{u}_1 + \mathbf{Z}_2\mathbf{u}_2 + \mathbf{Z}_3\mathbf{u}_3 + \mathbf{Z}_4\mathbf{u}_4 + \mathbf{e},$$

where \mathbf{y} is a vector of phenotypic performance values for an animal, \mathbf{X} is an incidence matrix relating a vector of fixed effects ($\boldsymbol{\beta}$) to the phenotypic records. \mathbf{Z}_1 , \mathbf{Z}_2 , \mathbf{Z}_3 , and \mathbf{Z}_4 are incidence matrices relating individual (sow) additive genetic effects (\mathbf{u}_1), maternal additive genetic effects (\mathbf{u}_2), permanent environment effects of the sow (\mathbf{u}_3), and the effects of service sire (\mathbf{u}_4) to the vector of records, \mathbf{y} ; and \mathbf{e} is a vector of random residual effects. The $\mathbf{E}(\mathbf{y}) = \mathbf{X}\boldsymbol{\beta}$, and the variance-covariance structure of the data was as follows:

$$\begin{bmatrix} \mathbf{u}_1 \\ \mathbf{u}_2 \\ \mathbf{u}_3 \\ \mathbf{u}_4 \\ \mathbf{e} \end{bmatrix} = \begin{bmatrix} \mathbf{A}\sigma_a^2 & & & & \\ & \mathbf{A}\sigma_{am}^2 & \mathbf{A}\sigma_m^2 & & \\ \mathbf{0} & \mathbf{0} & \mathbf{I}_c\sigma_c^2 & & \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{I}_g\sigma_g^2 & \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{I}_e\sigma_e^2 \end{bmatrix} \quad \text{Symmetric}$$

Fixed effects included in the models were covariates for inbreeding of the dam (sow) and the discrete effects of contemporary group (herd-year-season), type of litter allowed to nurse (pure or crossbred), and PSS genotype of the sow producing the record. Additionally, a fixed effect for parity and a NAT covariate were included in the model for analyzing SURV21. Parity was included as a fixed effect, and

Table 2. Reproductive trait means and best linear unbiased estimates of mean differences (\pm SE^a) between procine stress syndrome (PSS) normal (NN) and carrier (Nn) dams

Trait	Overall mean	Genotype contrast		<i>P</i> -value ^b	Difference required for <i>P</i> < .05, (.01) significance ^c	
		NN-Nn	\pm SE			
Adjusted no. born alive ^d	10.82	-.003	.14	.98	.27	(.36)
Adjusted no. at 21 d ^d	12.17	-.03	.05	.62	.10	(.13)
Adjusted 21-d litter weight, kg ^d	68.71	.45	.48	.35	.94	(1.24)
Survival to 21 d, %	95.48	.06	.44	.90	.86	(1.13)
Farrowing interval, d	172.0	.45	1.80	.80	3.53	(4.64)

^aStandard error of the difference between the genotype means.

^b*P*-values were calculated (SAS, 1996) using a two-tailed *t*-test (all differences were not significant).

^cRequired difference between NN and Nn females to reach *P* < .05 and *P* < .01 significance levels of a two-tailed *t*-test (SAS, 1996).

^dLandrace breed-specific adjustments (Brubaker et al., 1994).

previous 21-d litter weight, adjusted only for age at weighing, was included as a covariate in the model for the analysis of farrowing interval because no published adjustments for these traits were available.

The model was applied by mixed-model, multiple-trait DFREML procedures (MTDFREML) (Boldman et al., 1993). The relationship matrix was included in the animal model to account for the known variance-covariance structure that exists among additive breeding values of the animals evaluated. In total, 1,702 animals, 841 with records and 861 base animals, were included in the relationship matrix. Each herd was genetically tied, through related individuals, to at least one other herd such that all herds were connected. Contemporary groups within each herd were tied by one or more females. A contemporary group was defined as herd-year-season (**HYS**) of farrowing. To minimize the number of contemporary groups having fewer than five records, season was defined as four consecutive months. This method of defining contemporary groups resulted in the formation of 132 HYS groups. Contemporary groups were included as fixed effects in all models.

Each trait was individually analyzed and evaluated to the recommended convergence of the variance of the simplex function (Boldman et al., 1993). Models for each trait were "cold restarted" with previous variance-covariance values. Globally maximized convergence was determined when two successive evaluations produced the same (co)variances and $-2 \log$ likelihood of the simplex function (Boldman et al., 1993). Final estimates of the (co)variance components were used to obtain solutions for the mixed-model equations. Contrasts between NN and Nn PSS genotype for each trait were made by using the globally maximized parameters. Best linear unbiased estimates (**BLUE**) of the mean difference between PSS-NN and PSS-Nn sows were determined for each trait. The probability of a greater absolute *t* was calculated for each trait using statistical software from SAS (1996) and was used in declaring significant genotype differences.

Results and Discussion

Frequency of the PSS positive allele (*n*) ranged from .07 to .28 and averaged .13 in the breeding herd female population of the nine Landrace herds providing information for this study (Table 1). A chi-square analysis was performed to evaluate the distribution of dams within each PSS genotype. The observed PSS genotype distribution of dams within each herd did not differ from the expected distribution, given the PSS gene frequency within each herd. O'Brien (1995) reported *n* allele frequency estimates of .18, .21, and .22 in Landrace animals submitted for DNA testing from Canada, the United States, and England, respectively. Goodwin (1994) reported a .06 frequency of the PSS *n* allele of Landrace pigs involved with the National Barrow Show progeny test. Southwood et al. (1988) estimated an average PSS *n* allele frequency of .33 in 9 Landrace nucleus herds in United Kingdom.

There were no significant differences (*P* > .05) between NN and Nn dams for any of the traits analyzed (Table 2). Normal and Nn females had nearly identical adjusted NBA records. Adjusted number at 21 d was similar for NN and Nn sows. Though not significantly different, NN sows produced litters that averaged .45 kg heavier at 21 d than those of Nn sows. The average SURV21 was nearly identical for NN and Nn dams. Similarly, farrowing interval was only .44 d different (not significant) for NN and Nn dams.

The probability of a greater absolute *t* was calculated (SAS, 1996) for each trait and is presented in Table 2. Additionally, required differences to reach significance at *P* < .05 and *P* < .01 were calculated (SAS, 1996) for all traits using a two-tailed *t*-test and are illustrated in Table 2.

Previous European studies involving Landrace NN and Nn females reported results similar to those in the present study. Willeke et al. (1984) reported that NN, Nn, and nn German Landrace sows produced litters with similar NBA, number at 28 d, and mortality (survival) rate. Schneider et al. (1980) reported similar birth weights, mortality rates, and identical NBA for NN and Nn PSS genotypes in a

study involving Swiss Landrace sows. They reported that Nn sows had .11 more pigs ($P < .05$) at 28 d than did NN sows. Normal dams, however, produced litters 1.50 kg heavier ($P < .05$) at 28 d than did Nn dams.

Studies involving Belgian and British Landrace dams (Lampo et al., 1985; Simpson et al., 1986) have focused on comparisons between halothane positive (**HP**; PSS genotype nn) and halothane negative (**HN**; PSS genotypes NN or Nn) females. These studies generally reported HP sows to produce poorer litter weights at birth and 21 d but to have litters with NBA and NO21 similar to those of HN females.

Investigations involving other breeds or composite lines have yielded results somewhat contradictory to the present findings. Stalder (1995) found Nn females to have higher NB and NBA ($P < .05$) than NN females, but by 21 d NN females had higher NO21 and heavier LWT21 ($P < .05$) than Nn females in a study involving a composite line of stress-susceptible swine. Nystrom and Andersson (1993) reported that NN dams produced litters with heavier average pig weight at 21 d ($P < .05$) and similar NBA and NO21 compared with Nn sows in a study involving NN and Nn Yorkshire sows.

Studies involving a synthetic Hampshire-Pietrain line also focused on differences between HP and HN females (Webb and Jordon, 1978; Carden et al., 1985). Both studies reported HN sows to produce significantly ($P < .05$ or higher) higher NBA than HP females. Neither study found significant LWT21 differences between HP and HN dams.

Mabry (1977) found HN and HP sows to have similar NBA, NO21, LWT21, number of pigs per litter at 56 d, and survival rates to 56 d in a Yorkshire-based PSS-susceptible herd. There was some tendency for HP dams to produce poorer LWT21 compared with HN females. A long-term analysis of this herd (Stalder, 1995) found Nn females to have .94 more ($P < .05$) number born, 1.07 kg heavier ($P < .05$) litter birth weight, and .91 more ($P < .05$) adjusted number of pigs born alive compared with NN females. The litter weight of live pigs and survival rate from birth to transfer were not statistically different but tended to favor PSS Nn over NN females. By 21 d, results favored NN females, which had 2.86 kg heavier ($P < .05$) litter weights, 9.33% better ($P < .05$) survival rates from transfer to 21 d, and tended to have larger NO21 (not significant) compared with Nn females.

The results of this investigation suggest no statistical difference in the maternal performance of NN and Nn Landrace females. Research regarding the maternal performance of nn females and the greater postweaning death loss associated with nn animals (Webb et al., 1982) would seem to prevent the use of nn females in the breeding herd. Most commercial producers must decide whether to retain Nn females in their breeding herds. The negative effects of the PSS gene on quantitative and qualitative carcass traits, production traits, and mortality rates are well

documented and outlined by Christian and Mabry (1990). The results of this study suggest that commercial swine producers should consider factors other than maternal performance when making decisions concerning the use of the PSS gene in their breeding herd.

Implications

This research indicates no maternal performance difference between porcine stress syndrome-normal (PSS-NN) and carrier (Nn) Landrace sows. Hence, a swine producer's decision regarding the use of the PSS gene should be based on factors other than maternal performance. The molecular test for PSS allows producers to identify NN and Nn females. This study combined with previous research will allow producers to make an informed decision regarding the use of PSS-Nn females in their breeding herds.

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